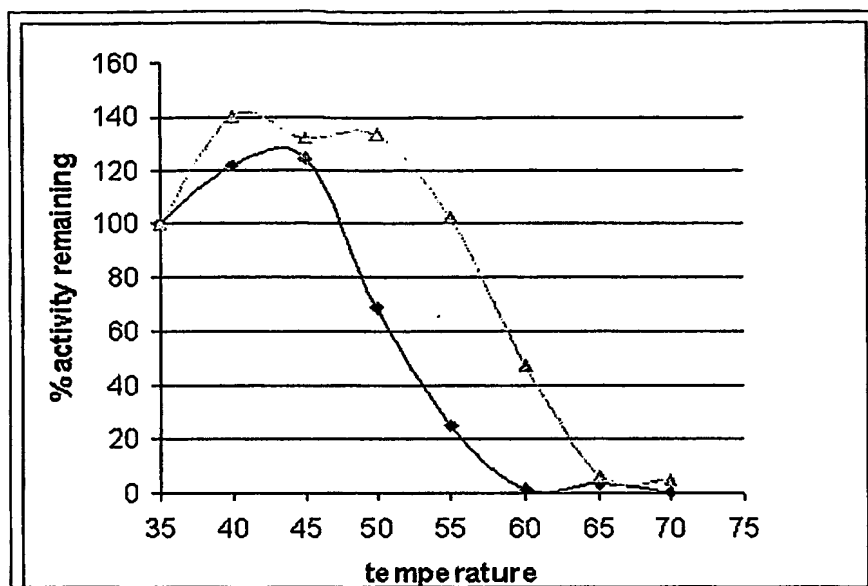
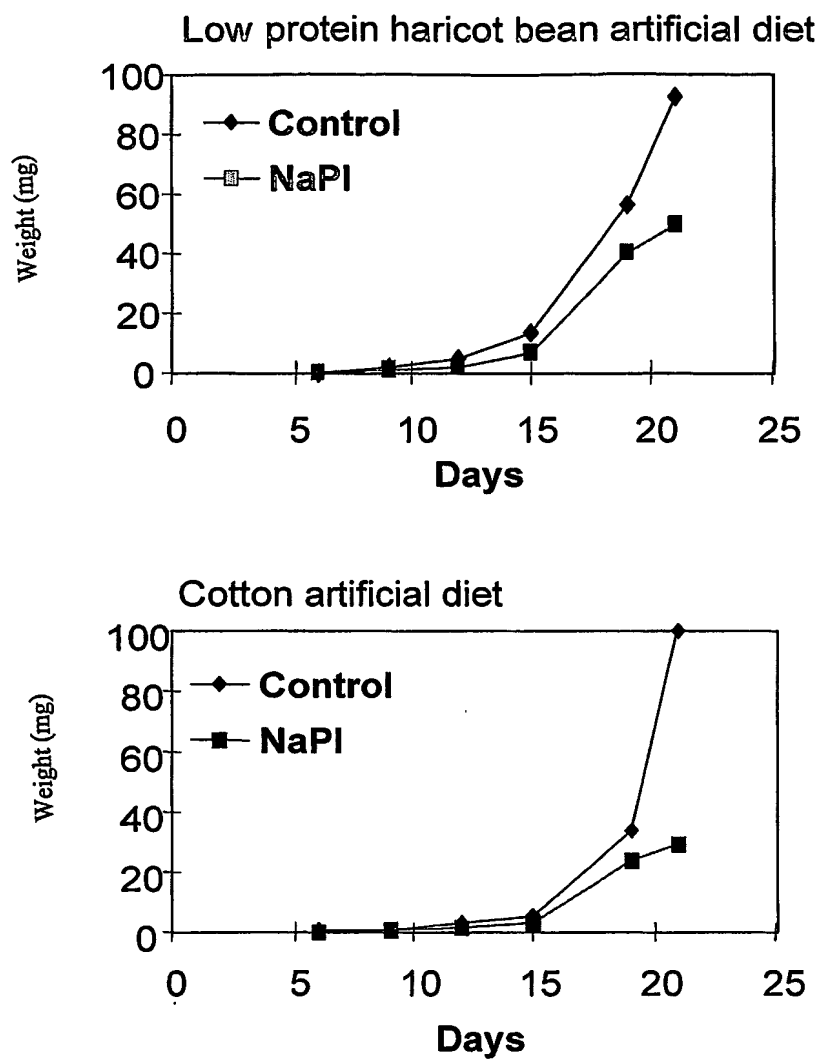


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**Figure 1**

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**Figure 2A**

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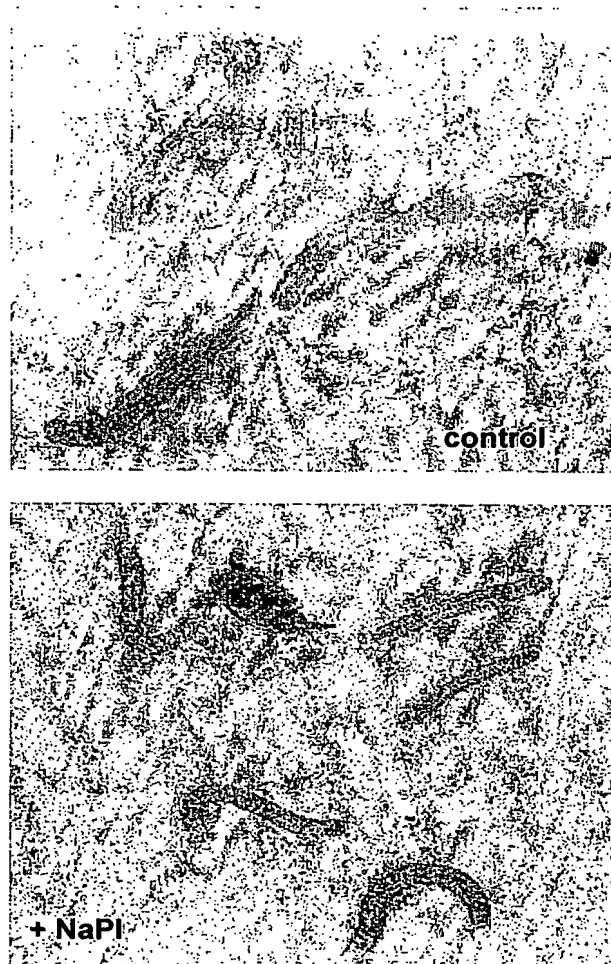
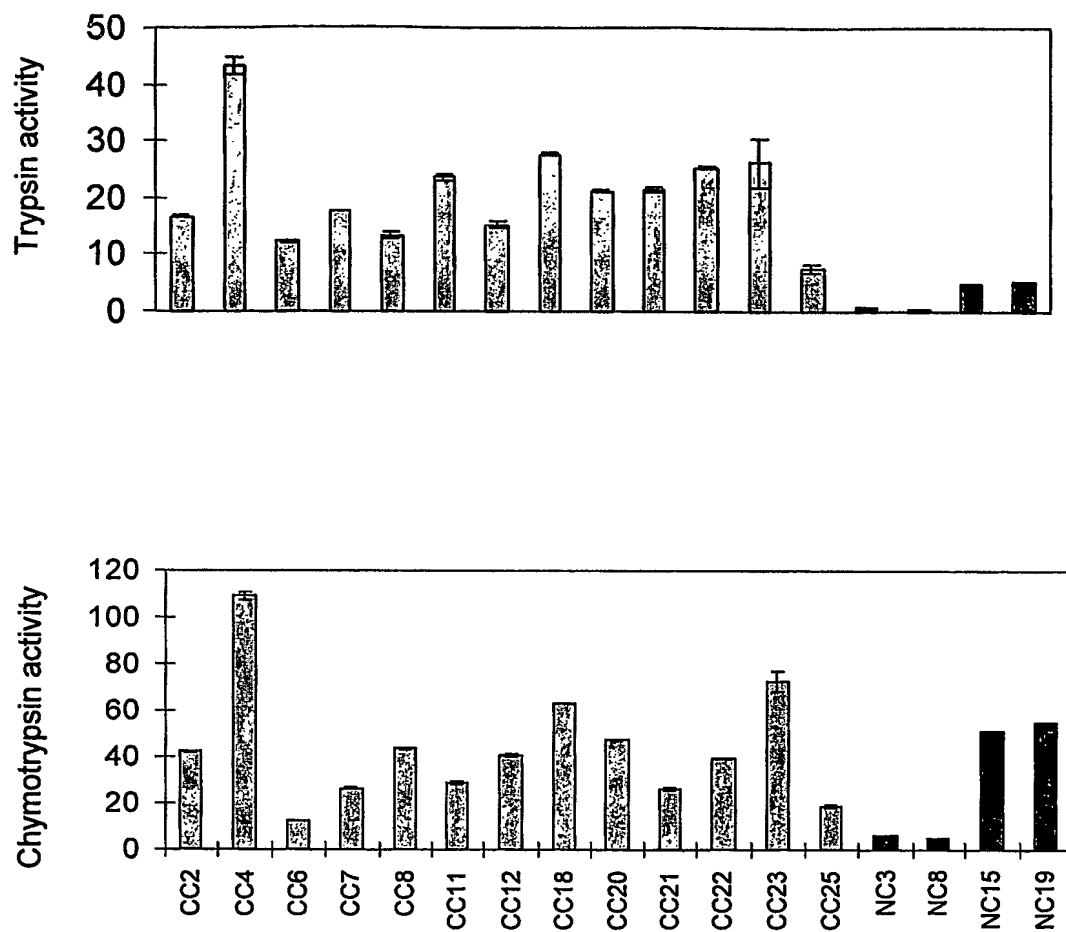


Figure 2B

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**Figure 2C**

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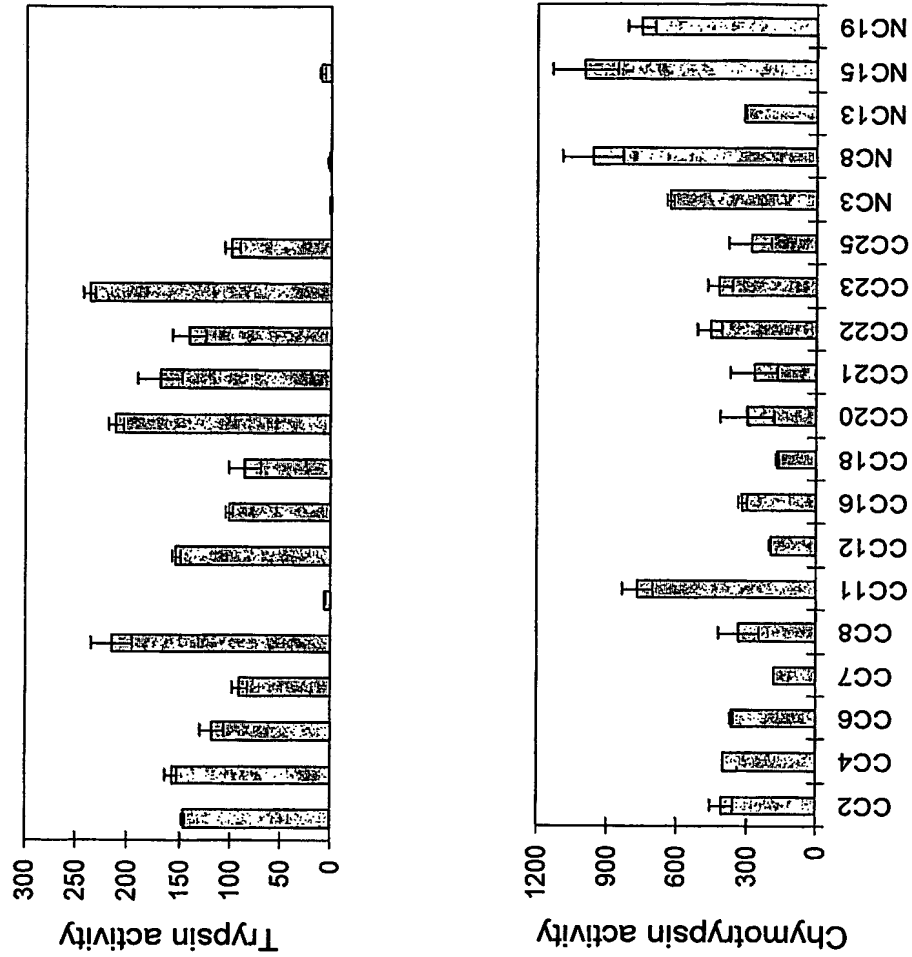
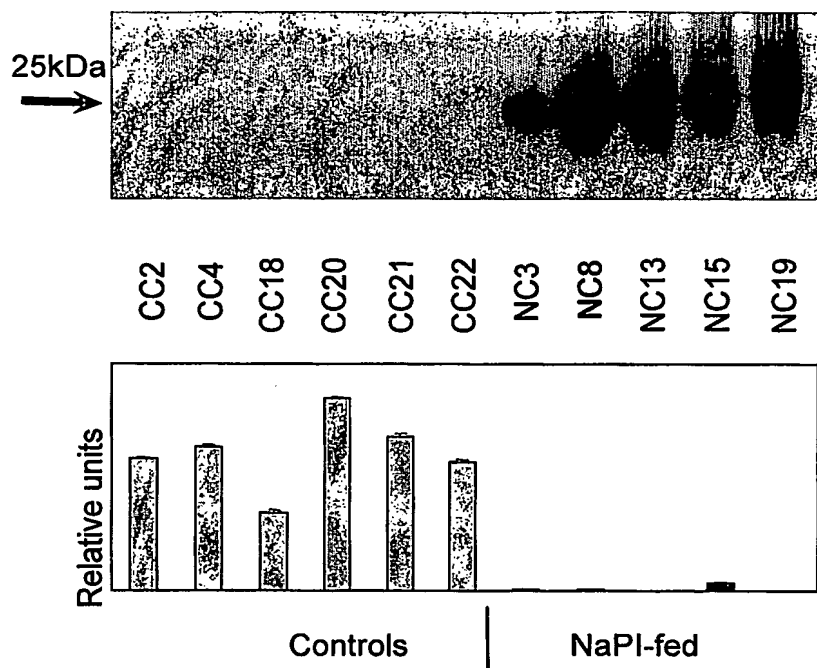
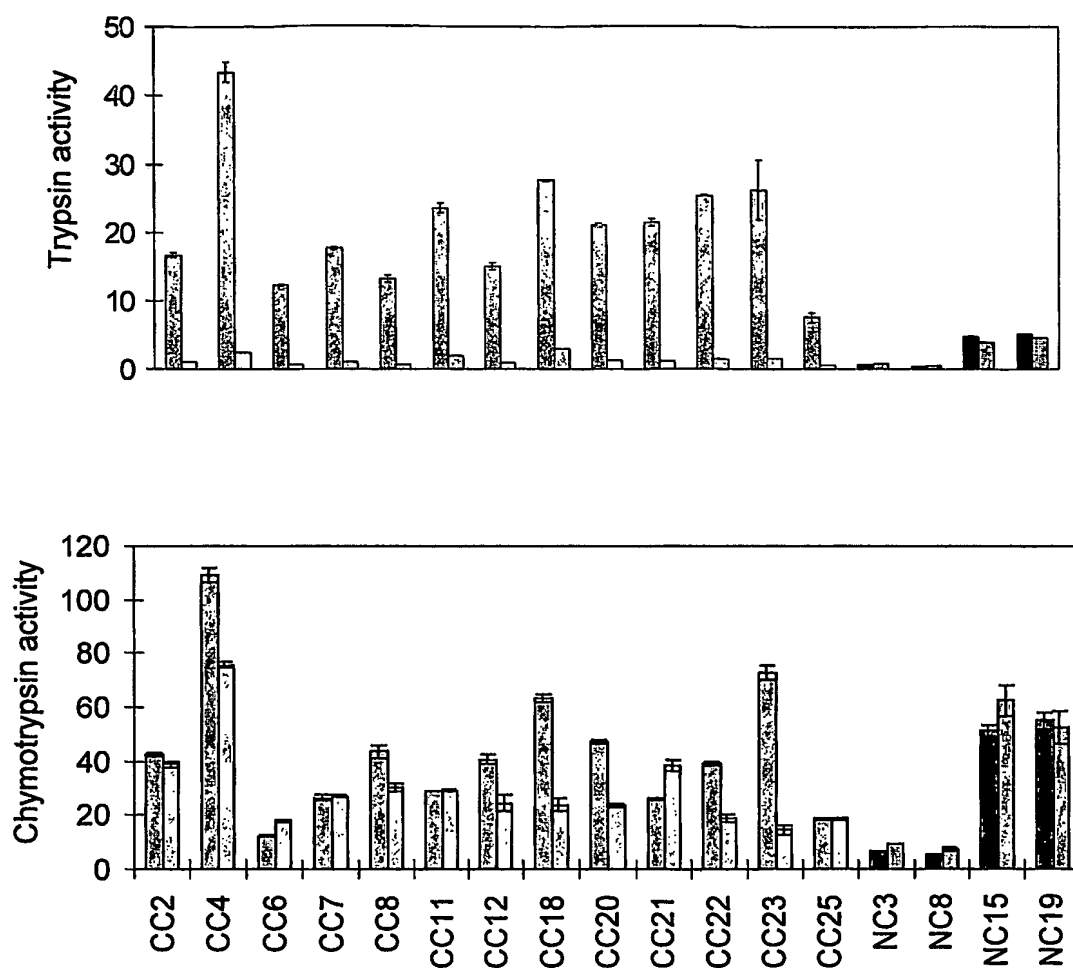


Figure 2D

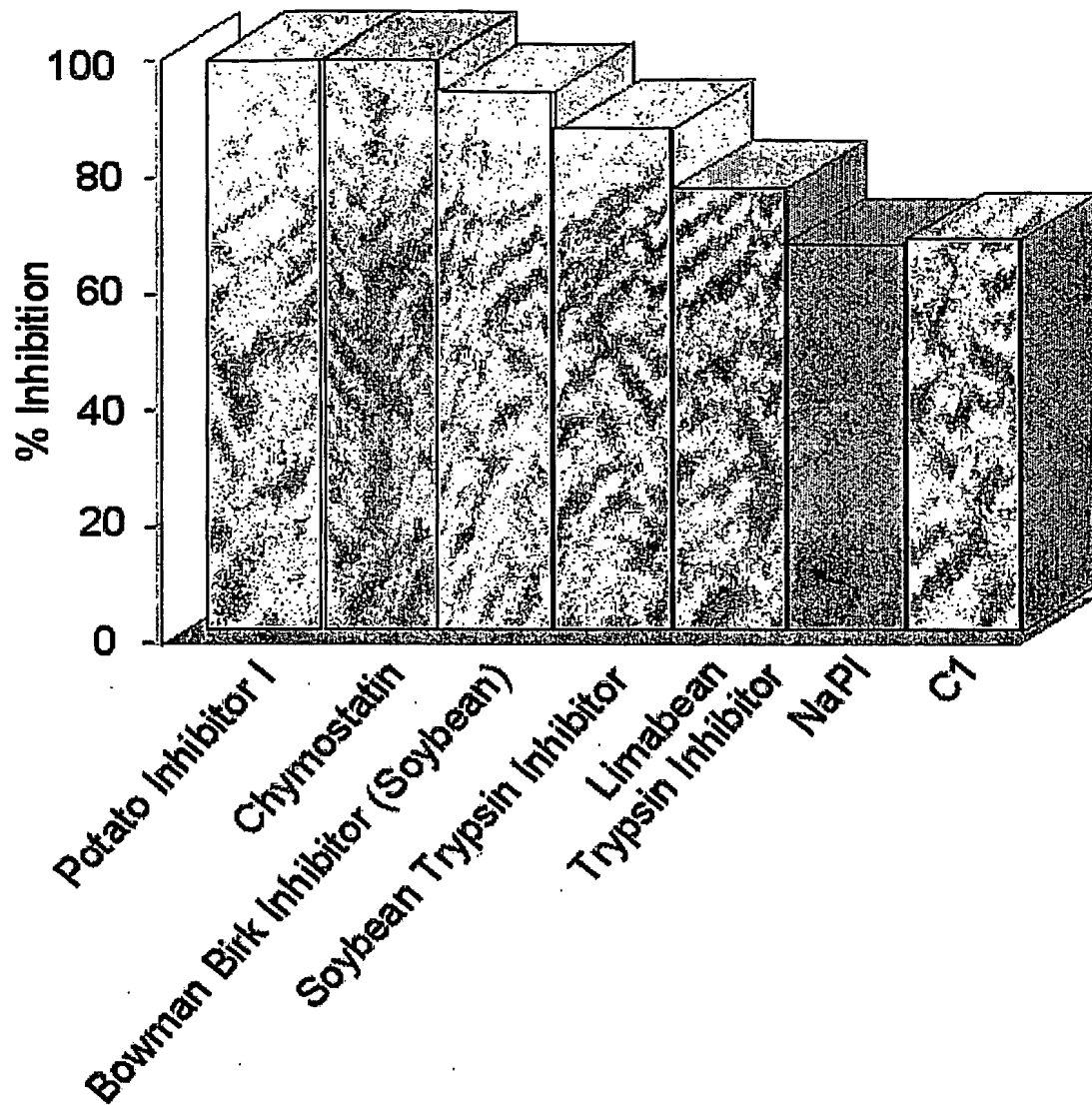
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**Figure 2E**

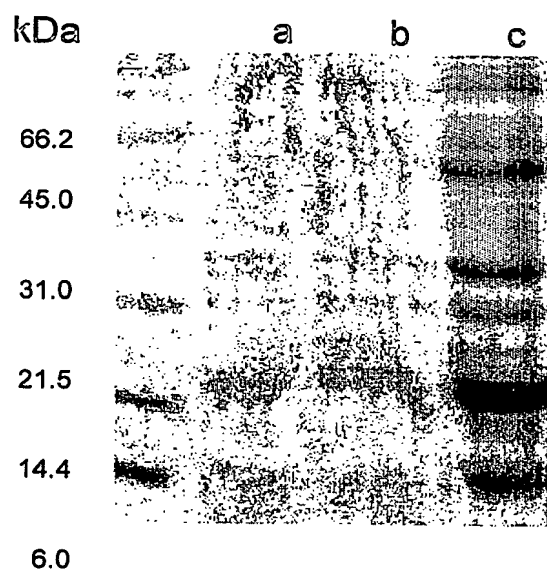
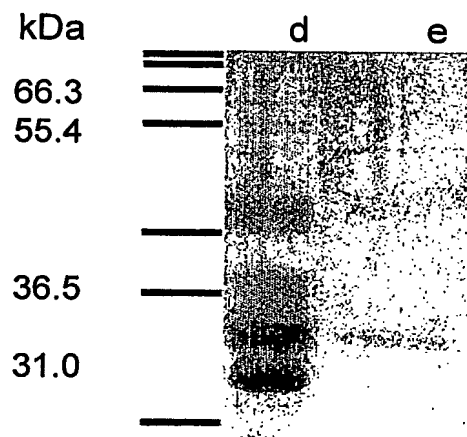
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**Figure 2F**

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**Figure 3**

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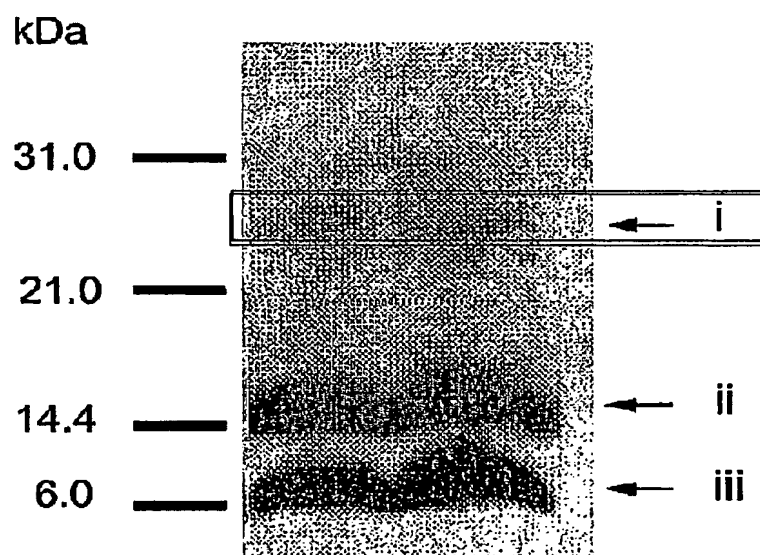
**Figure 4A****Figure 4B**

21.5
*Hp*CHY1 IVGGSTSSLGATPYQ

Figure 4C

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A

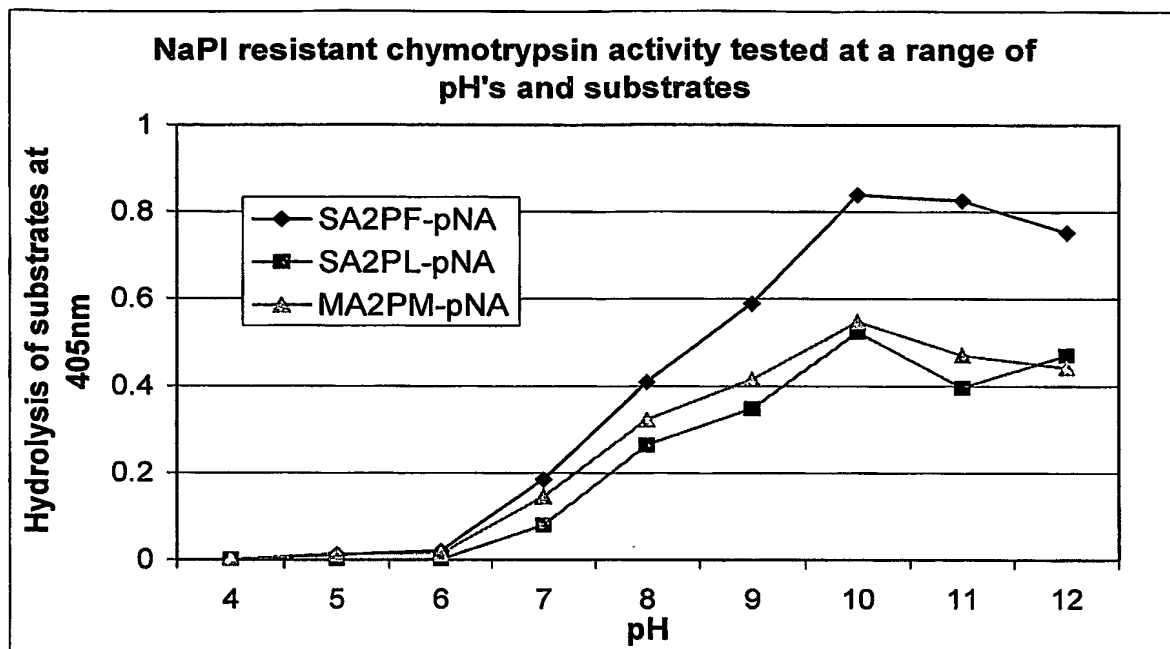


B

i	<i>Rech1a</i>	IVGGSLSVGQIPYQAGLVIDLAGGQAVCGGSLISA
	<i>Rech1b</i>	IVGGSISSIGQIPYGAGLVIDFAGGQAVC
	<i>Rech1c</i>	IVGGSTSSVGQFPYQAGLLASFAGGQAVC
	<i>Rech1d</i>	IVGGSVTTLDAYPTIAGLVYNFAGGQAVC

Figure 5

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**Figure 6**

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CAA72966 MKLLAVTLLAFAAVVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72959 ---LAVTLLAFAAVVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72960 MKLLAVTLLAFAAIVSARNIDLEDVIDLEDITAYDYHTKIGIPLAEKIRA
 CAA72958 -----INHEAVVDLEDITAYGYHTKVGIPLAEIIRI
 CAA72952 MKLFLGVCLTLAVAVSAVEIATPD----ADSPVFGYHAKFGIAEAARIKS
 CAA72951 -----

FWY79→ FWG1→

CAA72966 AEEEAERNPSRIVGGSTSSLGAFPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72959 AEEEAERNPSRIVGGSTSSLGAFPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72960 AEEEAERNPSRIVGGSSISLGAPYQAGLLATFASGQGVCGGSLLNNRRV
 CAA72958 AELEASRNPSRIVGGSSASLGAPYQAGLLINLPLGQSVCGGSLLNQRRV
 CAA72952 AEEVQSFNGQRIVGGSSITNIANVPYQAGLVITIFIFQSVCGASLISHNRL
 CAA72951 -----HNKWW

CAA72966 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNLIR
 CAA72959 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNLIR
 CAA72960 LTAAHCWFDGRNQARSFTVVLGSRVLFSGGTRLNTASVVMHGSWNPNLIR
 CAA72958 LTAAHCWFDGRNQANSLTVILGSINLYFGGTRLNSNSVVMHGSWNPNLIR
 CAA72952 VTAAHCKSDGVLANSFTVVLGSNTLFFGGTRINTNDVVMHPNWNPNATA
 CAA72951 LTAAHCLANRITFVVRFLTNLTRPEILVESANKYIHPDYDEIRAG-VQT

CAA72966 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGLARD
 CAA72959 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGLARD
 CAA72960 NDIAMINLPSNVATSGNIAP--IALPSGNELNNNFNGATAVASGFGLARD
 CAA72958 NDIAMINLPSNVGTSNNIAP--IALPSGNELNNQFAGFTATASGFGRTRD
 CAA72952 NDIAVLRIS--VSFSNVIQP--IALPSGDELNNLFVGANALASGFGRTRD
 CAA72951 ADLALVGLDHHIEYSANVQPSRLMSSAQKNINYE--GIQMIVSGFGRTRD

FWY72→

CAA72966 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRS
 CAA72959 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRG
 CAA72960 GGSVDGN---LRHVNLPVITNAVCTVSFP-GIIQSS-NICTSG--ANGRS
 CAA72958 GGSVSPT---LNHVNLPVITNNVCWQSFP-LYIQSS-NICTSG--ANGRS
 CAA72952 SGSIGTN-QQLSSVTIPVITNAQCAAVYGSGFVHAS-NICTSG--AGGKG
 CAA72951 LWNGGAASEILLWVYQRGVSNEECLRWYPTSQVIKEETICAGYWDNPSQS

←RVG4

CAA72966 TCQGDSSGGPLVVTSN-NRRILIGVTSFGSARGCQVGSPAAAFARVTSFISW
 CAA72959 TCQGDSSGGPLVVTSN-NRRILIGVTPFGSARGCQVGSPAAAFARVTSFISW
 CAA72960 TCQGDSSGGPLVVTSN-NRRILIGVTSFGSARGCQVGSPAAAFARVTSFISW
 CAA72958 TCQGDSSGGPLVVTSN-NRRILIGVTSFGSDRGCVGAPAAAFARVTSYISW
 CAA72952 TCNGDSSGGPLAVDSN-NRKILIGVTSYGAQAGCAAGFPAAAFARVTSFVDW
 CAA72951 SCQGDSSGGPLTIIDADGERTQVGIVSFGSTAGCNSPFPSGYVRPGHYHDW

←RVY72

CAA72966 INQRL-----
 CAA72959 INQRL-----
 CAA72960 INNLL-----
 CAA72958 INQRL-----
 CAA72952 VQSQ-----
 CAA72951 FTEVTGINFDWDSDAIIPGSSSESSSESSSEPSSESSSESSSEEDGANPSSS

CAA72966 -----
 CAA72959 -----
 CAA72960 -----
 CAA72958 -----
 CAA72952 -----
 CAA72951 EEDGSNPSSEEDAGSPPSEEEEEAPEKVRVVEY

Figure 7

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Primer Name	Sequence 5'-3'
FWG1	TCC CTT ACC AGG C (GCT) GTC [SEQ ID NO:38]
RVG4	TCT GGC GAA GGC AGC AGG [SEQ ID NO:39]
Y79Fw	CTG CTA GCC TCG GAC AAT TC [SEQ ID NO:40]
Y72Fw	CTG GAG TGC AGA CTG CTG AC [SEQ ID NO:41]
Y72Rv	GGA TGA TGG CGT CGC TGT CC [SEQ ID NO:42]

Figure 8

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HpF1Apcr	PYQAGL	VITIFIFQSVCGASLIPHNRLVTAAHCKSDGVLTAANSFTVVLGS	50
HpF1Bpcr	PYQAGL	VITIFIFQSVCGASLISHNRLVTAAHCKFDGVMTANSFTVVLGS	50
HpF2Apcr	PYQAGL	LANFASGQGVCGSLLNQRRVLTAAHCWFDGRNQARSFTVVLGS	50
HpF3pcr	ASLGQF	PYQAGLLINLPLGQSVCGSLLNQRRVLTAAHCWFDGRNQATSLTVILGS	57
HpF4pcr		-----	
HpF1Apcr		NTLFFGGTRINTNDVVMHPNWNPSTAANDIAVMRISS-VSFSNVIQPIAL	99
HpF1Bpcr		NTLFFGGTRINTNDVVMHPNWNPSTVANDIAVIRISS-IVFNNVIQPIAL	99
HpF2Apcr		VRLFSGGTRLDTASVVMHGSWNPNIIRNDIAMINLPSNVATSGNIAPIAL	100
HpF3pcr		INLFFGGTRLNSNSVVMHGSWNPNIIRNDIAIINLPSNVGTSGNIAPIAL	100
HpF4pcr		-----SGVQTADLALVGLDQEIEYSANVQPSRL	28
HpF1Apcr		PSGDELNNLFVGANALASGFGRTSDGGSIGSNQQ-VSSVTIPVITNDECA	148
HpF1Bpcr		PSGDELNNLFVGANALASGFGRTSDGGIGTNQQ-LSSVTIPVITNAECA	148
HpF2Apcr		PSGNELNNNFNGATATASGFGLARDGGSVDGN---LRHVNLPVITNAVCT	147
HpF3pcr		PSGNELNNQFAGFTATASGFGLTRDGGNVSP---LNHVNLPVITNNVCW	147
HpF4pcr		MSSAQKNINYEGIQMIVSGFGRTDDLWNGGAASEILLWVYQGVSNEECL	78
HpF1Apcr		AVYGS-AFVHSSNICTSGAGG--KGTCNGDSGGPLAIDSNN-EKILIGVT	194
HpF1Bpcr		AVYGP-AFVHDTNICTSGAGG--KGTCNGDSGGPLAVDSND-KKILIGVT	194
HpF2Apcr		VSFP--GIIQSSNICTSGANG--RSTCQGDSGGP-----	177
HpF3pcr		QSFP--LYIQSTNICTSGANG--RGTCQGDSGGPLVVTSSNN-RRILIGVT	192
HpF4pcr		RWYPTSQVIKEQTICAGYWDNPSQSSCQGDSGGPLTIIDADGERTQVGIV	128
HpF1Apcr		SYGAQAGCAAGLPAAFARK-----	213
HpF1Bpcr		SYGAADGCAAGFPAASPER-----	213
HpF2Apcr		-----	
HpF3pcr		SFGSDRGCVGAPAAAFAR-----	210
HpF4pcr		SFGSTAGCNSPFPSGYVRPGHYHDWFTEVTGINFDWDSDAIT	120

Figure 9

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HpCh1AI	---	---AVSA---	-VEIGTPDAD	SPVFGYHAKF	GIPEAARIKS	33
HpCh1BI	MKLFLGVCLA	LAVAVSA---	-VEIGTPEAG	SPVFGYHAKF	GIAEAARIKS	46
HpCh2A	MKLLAVTLLA	FAAVVSARNI	DLEDVIDLED	ITAYDYHTKI	GIPLAEEIRA	50
HpCh2B	MKLLAVTLLA	FAAVVSARNI	DLEDVIDLED	ITAYDYHTKI	GIPLAEKIRA	50
HpCh3A	-----	-----	-----	-----	-----	-----
HpCh4I	MAAAYLLGLL	FVLGYVQGGL	LNADPAIIED	LRDA-----	-----	34
HpCh4II	MAAAYLLGLL	FVLGYVQGGL	LNADPAIIED	LRDA-----	-----	34
		↓↓			⊙	
HpCh1AI	AEEVQSFNGQ	RIVGGSITDI	ANVPYQAGLV	ITIFIF-QSV	CGASLISHNR	82
HpCh1BI	AEEVQSFNGQ	RIVGGSITNI	ANVPYQAGLV	ITIFIF-QSV	CGASLISHNR	95
HpCh2A	AEEEEERDPS	RIVGGSTSSL	GAFPYQAGLL	ANFASG-QGV	CGGSLLNQRR	99
HpCh2B	AEEEEERNPS	RIVGGSTSSL	GAFPYQAGLL	ASFASG-QGV	CGGSLLNVRR	99
HpCh3A	-----	-IVGSSASL	GQFPYQAGLL	INLPLG-QSV	CGGSLLNQRR	38
HpCh4I	--EFSSG--S	RIVAGWPAVE	GQIPYQGSRL	MVSAIGGVSS	CGCSLIHNKW	80
HpCh4II	--EFSSF--S	RIVAGWPAVE	GQIPYQGSRL	MVSAIGGVSS	CGCSLIHNKW	80
	▼●					
HpCh1AI	LVTAAHCKSD	GVLTRANSFTV	VLGSNTLFFG	GTRINTNDVV	MHPNWNPS--	130
HpCh1BI	LVTAAHCKFD	GVMTANSFTV	VLGSNTLFFG	GTRINTNDVV	MHPNWNPS--	143
HpCh2A	VLTAACHWFD	GRNQARSFTV	VLGSVRLFSG	GTRLDTASVV	MHGSWNPN--	147
HpCh2B	VLTAACHWFD	GRNQARSFTV	VLGSVRLYSG	GTRLNTASVV	MHGSWNPN--	147
HpCh3A	VLTAACHWFD	GRNQATSLTV	ILGSINLFFG	GTRLNNSNVV	MHGSWNPN--	86
HpCh4I	VLTAAHCLAN	----RITFVV	RFGLTNLTRP	EILVESTNKY	IHPEYDEIRA	126
HpCh4II	VLTAAHCLAN	----RITFVV	RFGLTNLTRP	EILVESTNKY	IHPEYDEIRA	126
	▼					
HpCh1AI	-TAANDIAVM	RISS-VSFSN	VIQPIALPSG	DELNNLFVGA	NALASGFGRT	178
HpCh1BI	-TVANDIAVI	RISS-IVYNN	VIQPIALPSG	DELDNLFVGA	NALASGFGRT	191
HpCh2A	-LIRNDIAMI	NLPSNVATSG	NIAPIALPSG	NELNNNFNGA	TATASGFGLA	196
HpCh2B	-LVRNDIAMI	NLPSNVATSG	NIAPIALPSG	NELNNQFAGA	TATASGFGLA	196
HpCh3A	-LIRNDIAII	NLPSNVGTSG	NIAPIALPSG	NELNNQFAGF	TATASGFGLT	135
HpCh4I	GVQTADLALV	GLDHEIEYSA	NVQPSRLMSS	AQKNINYEGI	QMIVSGFGRT	176
HpCh4II	GVQTADLALV	GLDQEIEYSA	NVQPSRLMSS	AQKNINYEGI	QMIVSGFGRT	176
			●	●		
HpCh1AI	SDGGSIGSNQ	Q-VSSVTIPV	ITNDECAAVY	GS-AFVHSSN	ICTSGAGG--	224
HpCh1BI	SDSGGIGTNQ	Q-LSSVTIPV	ITNAECAAVY	GP-AFVHDTN	ICTSGAGG--	237
HpCh2A	RDGGSVDGN-	--LRHVNLPV	ITNAVCTVSF	P--GIIQSSN	ICTSGANG--	239
HpCh2B	RDGGVIDGN-	--LRHVNLPV	ITNAVCSQSF	P--GLIQASN	VCTSGANG--	239
HpCh3A	RDGGNVSPN-	--LNHVNLPV	ITNNVCWQSF	P--LYIQSTN	ICTSGANG--	178
HpCh4I	DDLWNGGAAS	EILLWVYQRG	VSNEECLRWY	PTSQVIKEQT	ICAGYWDNPS	226
HpCh4II	DDLWNGGAAS	EILLWVYQRG	VSNEECLRWY	PTSQVIKEQT	ICAGYWDNPS	226
	¥ ● ▼		§	●	#	
HpCh1AI	KGTCNGDSGG	PLAVDSNNEK	IL-IGVTSYG	AQAGCAVG--	---LPAAFAR	268
HpCh1BI	KGTCNGDSGG	PLAVDSNDKK	IL-IGVTSYG	AADGCAAG--	---FPAAFAR	281
HpCh2A	RSTCQGDSGG	PLVVNSNNRR	IL-IGVTSFG	SARGCQVG--	---SPAAFAR	283
HpCh2B	RSTCQGDSGG	PLVVNSNNRR	IL-IGVTSFG	SARGCQVG--	---SPAAFAR	283
HpCh3A	RGTCQGDSGG	PLVVTNNRR	IL-IGVTSFG	SDRGCVG--	---APAAAFAR	222
HpCh4I	QSSCQGDSGG	PLTIIDADGE	RTQSRYCELR	--IHCWNA--	-AHSPQGYVR	272
HpCh4II	QSSCQGDSGG	PLTIIDADGE	RTQVGIVSSD	PLLDATVHSP	RVTSPGHYHD	276
HpCh1AI	VTSFVSWVQS	Q-----	-----	-----	-----	279
HpCh1BI	VTSFVSWVQS	Q-----	-----	-----	-----	292
HpCh2A	VTSFISWINQ	RL-----	-----	-----	-----	295
HpCh2B	VSSYISWINQ	RL-----	-----	-----	-----	295
HpCh3A	VTSYISWINQ	RL-----	-----	-----	-----	295
HpCh4I	PGHYHDWLTE	VTGINFDWDS	DAIIP-----	-----	-----	234
HpCh4II	GHRGDRHQLR	LGQRRHYPDS	SESSLRAAIL	PLESSRAFIR	RNOSSFRGGL	297
						326

Figure 10A

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HpCh1AI	-----	-----	-----	-----	279
HpCh1BI	-----	-----	-----	-----	292
HpCh2A	-----	-----	-----	-----	295
HpCh2B	-----	-----	-----	-----	295
HpCh3A	-----	-----	-----	-----	234
HpCh4I	-----	-----	-----	-----	297
HpCh4II	CQPPRFPTRT	VPTHLPRRTL	AAPPSEEEEA	PEKVRVVEY	365

Figure 10B

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		F1	F2
[SEQ ID NO:55]	<i>Rech1a</i>	IVGGSLSSVG	QIEFYQAGLVI
[SEQ ID NO:56]	<i>Rech1b</i>	IVGGSTSSVG	QFPYQAGLLA
[SEQ ID NO:57]	<i>Family1a</i>	IVGGSITDIA	NVPYQAGLVI
[SEQ ID NO:58]	<i>Family1b</i>	IVGGSITNIA	NVPYQAGLVI
[SEQ ID NO:59]	<i>Family2a</i>	IVGGSTSSLG	AFPYQAGLLA
[SEQ ID NO:60]	<i>Family2b</i>	IVGGSTSSLG	AFPYQAGLLA
[SEQ ID NO:61]	<i>Family3</i>	IVGGSSASLG	QFPYQAGLSL
[SEQ ID NO:62]	<i>Family4</i>	IVAGWPAVEG	QIPYQGSLRM

Figure 11A

N-terminal sequence of resistant chymotrypsin (Rech 1a)	
IVGGSLSSVGQIEFYQAGLVIDLAGGQAVCGGSLISA [SEQ ID NO:9]	
Primer Name	Oligonucleotide sequence 5'-3'
Fw2ResChy = F1	TC(AGCT) GT(AGCT) GG(AGCT) CA(AG) AT(ACT) CC [SEQ ID NO:10]
FwResChym = F2	GT(AGCT) AT(ACT) GA(CT) CT(AGCT) GC(AGCT) GG(AGCT) GG [SEQ ID NO:11]

Figure 11B

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HpCHF5 GTTCACCTCGAGGATTCTATTGATCTGGAAGATATTACCGCTTGGGGATA 50
 V H L E D S I D L E D I T A W G Y
 -40 -24
HpCHF5 CCTCACCAAATTCGGTATTCCAGAAGCTGAGAAAATCCGCAACGCTGAAG 100
 L T K F G I P E A E K I R N A E
 -8
HpCHF5 AAGCTAGCTCTGCTAGCAGGATCGTCGGTGGTTTCATTGTCCAGTGTCCGA 150
 E A S S A S R A L V G G S L S S V G
 -1 +1 +10
HpCHF5 CAGATCCCTTACCAGGCTGGTCTCGTCATTGACTTAGCAGGTGGCCAGGC 200
Q T P Y E O A G L V I D L A G G T O R A
HpCHF5 TGTCTGCGGAGGCTCCCTGATCAGCGCTTCCCGCTACTGACCGCTGCTC 250
V C G G S V L S A S R V L T A A
HpCHF5 ACTGCTGGTTCGACGGCCAAACCAGGCCTGGAGATTACCGTTGTTCTT 300
 H C W F D G Q N Q A W R F T V V L
 #
HpCHF5 GGTTCACCACCTTGTTCTCTGGCGGTACCAGAATCCCTACATCCAATGT 350
 G S T T L F S G G T R I P T S N V
HpCHF5 TGTTATGCACGGAAGCTGGACTCCTAGCCTTATCCGTAACGATGTTGCCG 400
 V M H G S W T P S L I R N D V A
 #
HpCHF5 TAATCAGATTGGGCACCAACGTAGCAACCTCAAACACCATTGCCATCATC 450
 V I R L G T N V A T S N T I A I I
HpCHF5 GCTCTACCCAGCGGCAGCCAGATCAACGAGAACTTCGCCGGTGAAACCGC 500
 A L P S G S Q I N E N F A G E T A
HpCHF5 CCTCGCCTCCGGCTTCGGTCTCACCAGTGACACCGGCAGCATCTCCAGCA 550
 L A S G F G L T S D T G S I S S
HpCHF5 ACCAGGCTCTGAGCCACGTCAACCTGCCAGTGATACCAACGCTGTGTGC 600
 N Q A L S H V N L P V I T N A V C
HpCHF5 AGAAATTCATTCCCCCTGCTGATCCAGGACTCTAACATTTGCACCAGCGG 650
 R N S F P L L I Q D S N I C T S G
HpCHF5 TGCCAACGGCAGGAGCACTTGCCGCGGTGACTCCGGCGGTCTCTCGTCCG 700
 A N G R S T C R G D S G G P L V
 S #
HpCHF5 TCACCAGGAACAACAGACCACTCTTGATCGGTATCACCTCTTTCCGGATCT 750
 V T R N N R P L L I G I T S F G S
HpCHF5 GCCCGCGGTTGCCAAGTTGGATCTCCCGCTGCCTTCGCCAGAGTCACCTC 800
 A R G C Q V G S P A A F A R V T S
HpCHF5 TTACATCAGCTGGATCAACGGCCAGCTCTAAAATATCGAACATTTTGCCA 850
 Y I S W I N G Q L *
HpCHF5 TATCTACAGAGATATTTTGAAATACGTTAATTTAAATAAATATTTTATTT 900
HpCHF5 ATTCAAAAAAAAAAAAAAAAAA 921

Figure 12

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HpCh1AI	IVGGSIITDIANVPYQAGLVITIFI-FQSVCGASLISHNRIVTAAHCKSDG	49
HpCh1BI	IVGGSIITNIANVPYQAGLVITIFI-FQSVCGASLISHNRIVTAAHCKFDG	49
HpCh2A	IVGGSTSSLGAFPYQAGLEAFAS-GQVCGGSLINQRRVLTAAHCFDG	49
HpCh2B	IVGGSTSSLGAFPYQAGLASFAS-GQVCGGSLINQRRVLTAAHCFDG	49
HpCh3	IVGGSSASLGQFPYQAGSLIYS--GQSVCGGSLINQRRVLTAAHCFDG	48
HpCh4I	IVAGWPAVEGQIPYQGSIRMVSAIGFVSSGCSLTHNKWVLTAAHCLAN-	49
HpCh5	IVGGSLSSVGQIPYQAGLVITDLAG-GQAVCGGSLISASRVLTAAHCFDG	49
TrypsinIV	IVGGYTCEENSIPYQVSLNSGSH-----FCGGSLISEQWVVSAAHCY----	42
HpCh1AI	VLTANSFTVVLGSNTLFFGG-TRINTNDVVMHPNWNPS---TAANDIAYM	95
HpCh1BI	VMTANSFTVVLGSNTLFFGG-TRINTNDVVMHPNWNPS---TVANDIAYI	95
HpCh2A	RNQARSFTVVLGSVRLFSGG-TRIDTASVVMHGSWNPN---LIRNDIAMI	95
HpCh2B	RNQARSFTVVLGSVRLFSGG-TRINTASVVMHGSWNPN---LVRNDIAMI	95
HpCh3	RNQATS LTVILGSINLFFGG-TRINSNSVVMHGSWNPN---LIRNDIATI	94
HpCh4I	---RITFWVRFLTNLTRPE-ILVESTNKYTHPEYDEIRAGVQTADLALV	95
HpCh5	QNQAWRFTVVLGSITLFSGG-TRIPTSNVVMHGSWNTPS---LIRNDIAYI	95
TrypsinIV	-KTRIQVRLGEHNLIKVLEGEQFTNAAKTIRHPKYNRD---TLDNDIMET	88
HpCh1AI	RISS-VSFSNVITQPIALPSGDELNNLFVGANALAFGFGRTSDGGSTGSNQ	144
HpCh1BI	RISS-IVYNNVITQPIALPSGDELNNLFVGANALASGFGRTSDGGSTGTNQ	144
HpCh2A	NLPSNVATSGNIAPIALPSGNELNNNFAGATATASGFGGLARDGGSVQGN-	144
HpCh2B	NLPSNVATSGNIAPIALPSGNELNNQFAGATATASGFGGLARDGGVLDGN-	144
HpCh3	NLPSNVGTSGNIAPIALPSGNELNNQFAGFTATASGFGGLTRDGGNVSP-	143
HpCh4I	GLDHEITEYSANVQPSRLMSSAQKNINYEIQMTIVSGFGRTDDLWNGGAAS	145
HpCh5	RLGTNVATSNITATIALPSGSQINENFAGETALASGFGGLTSDTGSTSSNQ	145
TrypsinIV	KLSSPAVINARVSTISLPIAP-----PAAGTECLISGWCNTLSFGADYPD-	133
HpCh1AI	Q-VSSVITIPVITNDECAAVYG-SAFVHSSNICT--SGAGCKGTCNGDSGG	190
HpCh1BI	Q-LSSVITIPVITNAECAAVYG-PAFVHDINICT--SGAGCKGTCNGDSGG	190
HpCh2A	--LRHVNIPVITNAVCTVSE--PGIIQSSNICT--SGANGRSTCQGDSSG	188
HpCh2B	--LRHVNIPVITNAVCSQSE--PGLIQASNVCT--SGANGRSTCQGDSSG	188
HpCh3	--LNHVNIPVITNNVCWQSF--PLYIQSSNICT--SGANGRSTCQGDSSG	187
HpCh4AI	EILLWVYQRGVSNEECLRWYPTSQVIKEQTICAGYWDNPSSSCQGDSSG	195
HpCh5	A-LSHVNIPVITNAVCRNSE--PLLIQDSNICT--SGANGRSTCRGDSSG	190
TrypsinIV	E-LKCEAPVLTQAECKASY--PGKITNSMFCVG-FLEGGKDSQORDSSG	179
HpCh1AI	PLAIDSNN--EKILIGVTSYGAQAGCAAGLPAAAFARVTSFVSWVQSQ---	235
HpCh1BI	PLAIVSND--KKILIGVTSYGAADGCAAGFPAAAFARVTSFVSWVQSQ---	235
HpCh2A	PLVVNSNN--RRILIGVTSFGSARGCQVGS PAAAFARVTSFISWINQRI---	234
HpCh2B	PLVVNSNN--RRILIGVTSFGSARGCQVGS PAAAFARVSSYISWINQRI---	234
HpCh3	PLVVTSNN--RRILIGVTSFGSDRGCVGAPAAAFARVTSYISWINQRI---	233
HpCh4I	PLTUIDADGERTQSRYCELRHCWNATAHSPQGYVRPGHYHDWFTEVTGI	245
HpCh5	PLVVTRNN--RPLLIGITSGSARGCQVGS PAAAFARVTSYISWINGQL---	236
TrypsinIV	PVMCNG-----QLQGVSWGHGCAWK-N-RPGVYTKVYNYVDWIKDTIAA	222
HpCh1AI	-----	235
HpCh1BI	-----	235
HpCh2A	-----	234
HpCh2B	-----	234
HpCh3	-----	233
HpCh4I	NFDWDSDAIIP	256
HpCh5	-----	236
TrypsinIV	NS-----	224

Figure 13

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[SEQ ID NO:71]	DH04_H02 ARMIGERA	VHLEDSDLE	DITAWGYLTK	FGIPEAEKIR	NAEEASSASR
[SEQ ID NO:72]	RECH1A PUNCTIGERA
	DH04_H02 ARMIGERA	IVGGSLSLQ	QIPYQAGLVI	DLSGGQAVCG	GSLISASRVL
	RECH1A PUNCTIGERAA.....
	DH04_H02 ARMIGERA	TAAHCWFDGQ	NQAWRFTVVL	GSTTLFSGGT	RIATSNVVMH
	RECH1A PUNCTIGERAP.....
	DH04_H02 ARMIGERA	GSWTPSLIRN	DVAVIRLGTN	VGTSNTIAII	ALPSGSQINE
	RECH1A PUNCTIGERA
	DH04_H02 ARMIGERA	NFAGETALAS	GFGLTSDSGS	ISSNQALSHV	NLPVITNAVC
	RECH1A PUNCTIGERAT..
	DH04_H02 ARMIGERA	RSSFPLLIQD	SNICTSGANG	RSTCRGDSGG	PLVVTRNSRP
	RECH1A PUNCTIGERA	.N.....N..
	DH04_H02 ARMIGERA	LLIGITSFGS	ARGCQVGSPA	AFARVTSYIS	WINGQ
	RECH1A PUNCTIGERA

Figure 14

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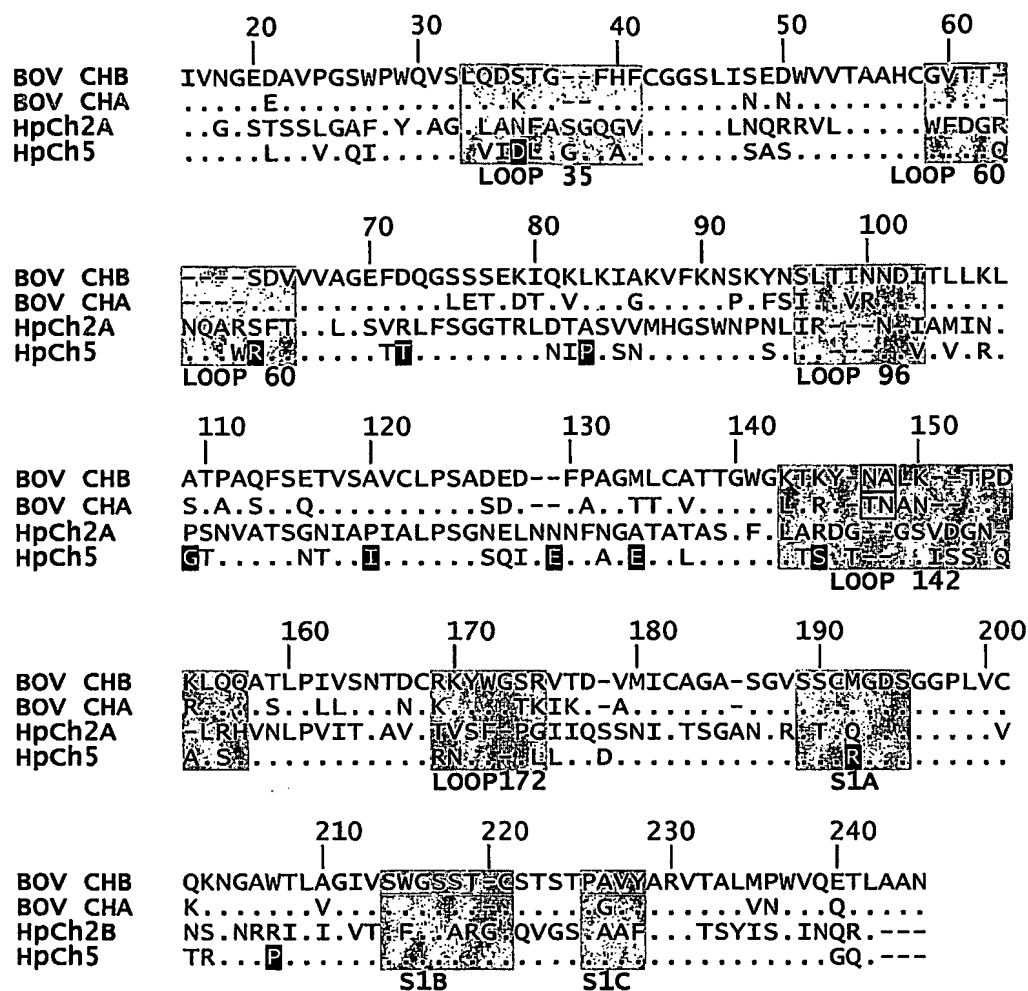


Figure 15

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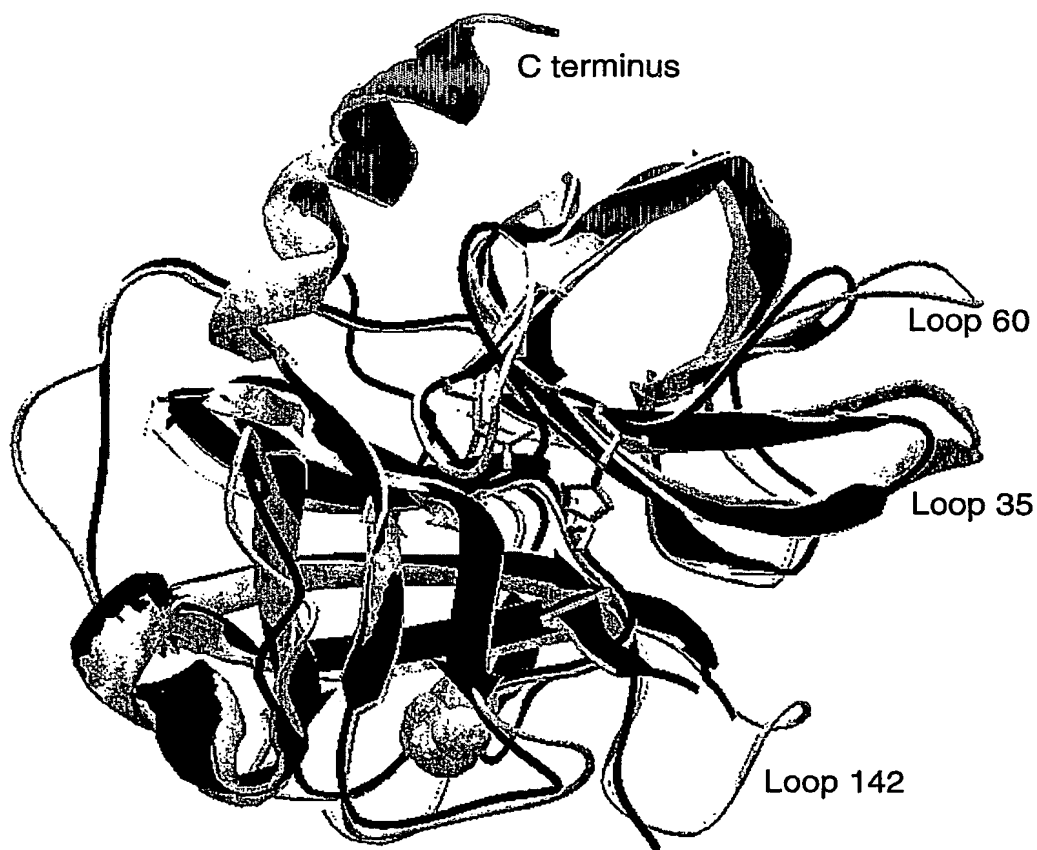


Figure 16

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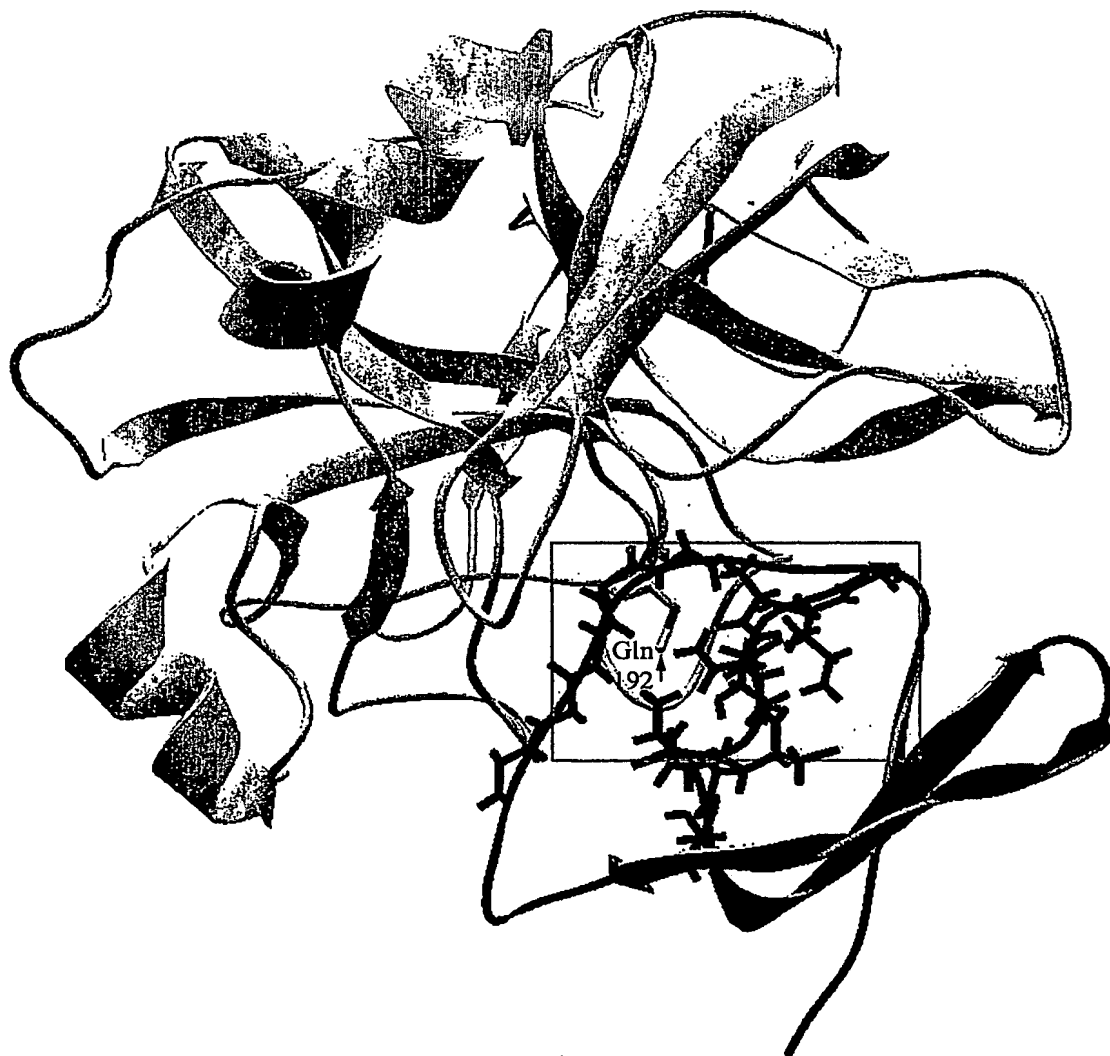


Figure 17

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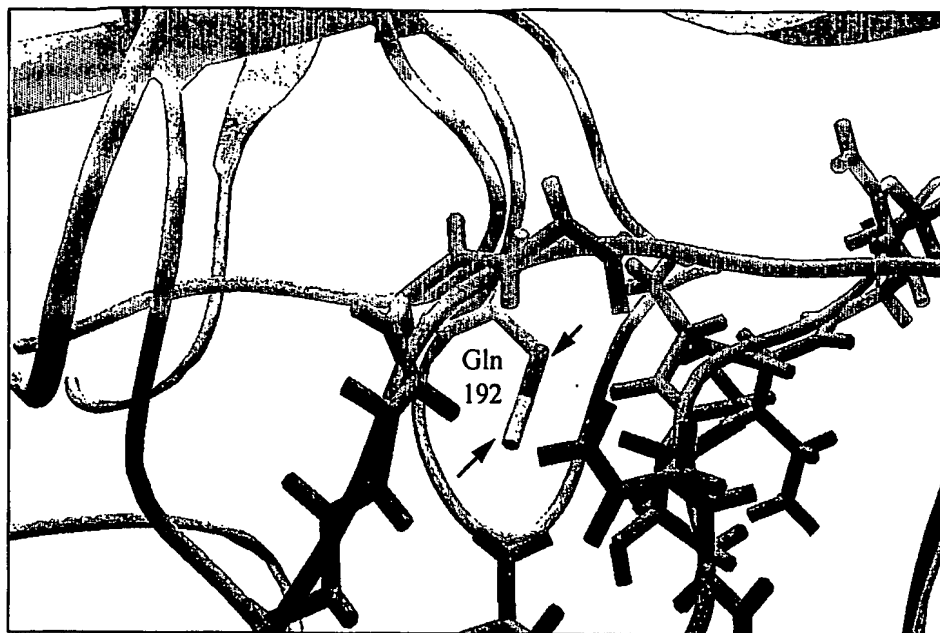


Figure 18A

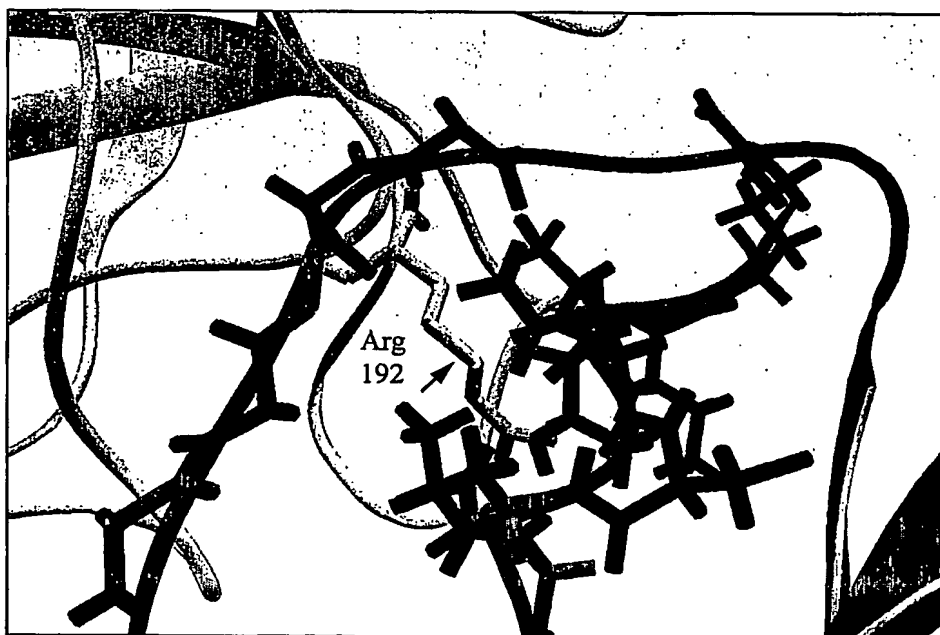


Figure 18B

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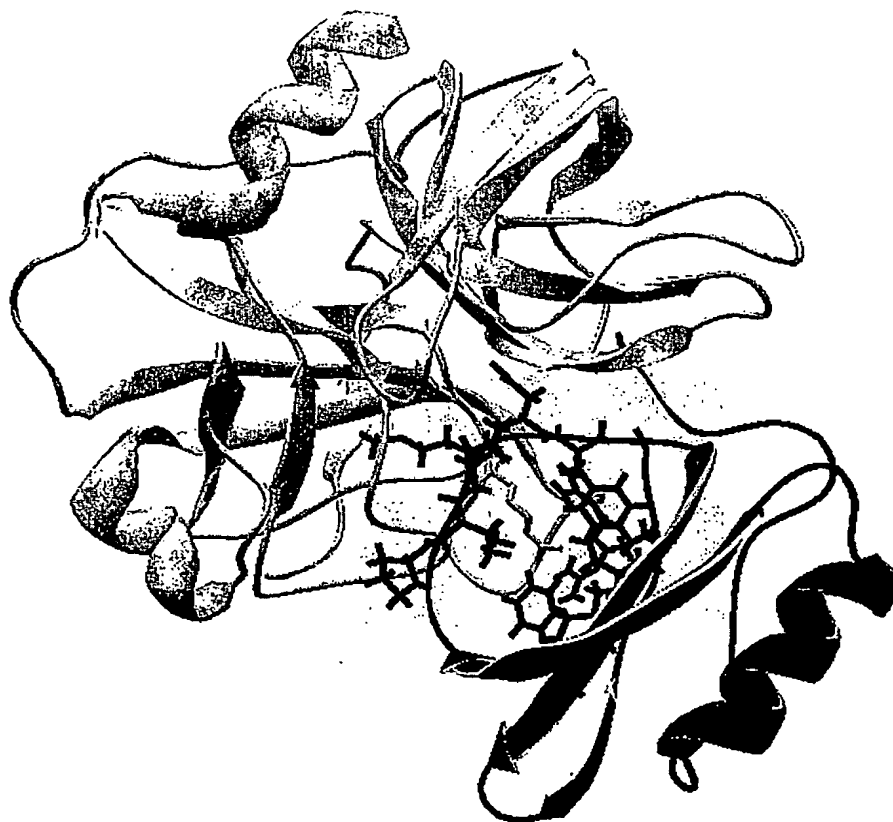


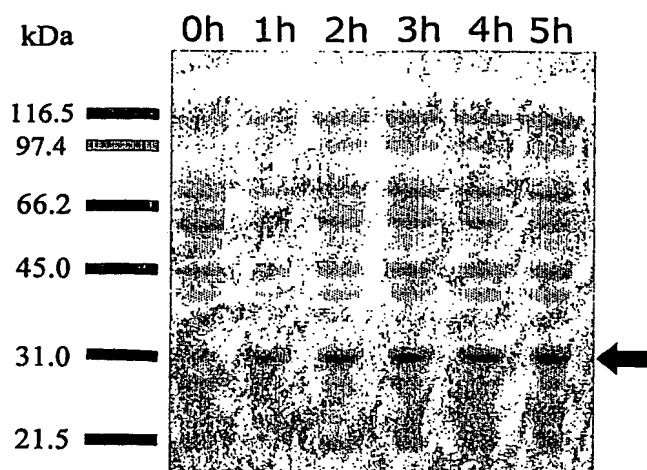
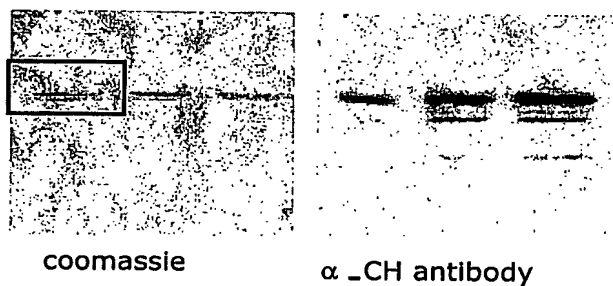
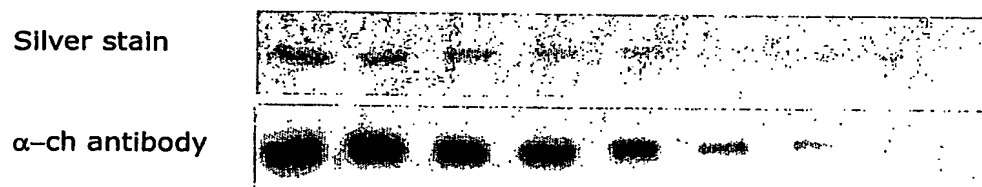
Figure 19A

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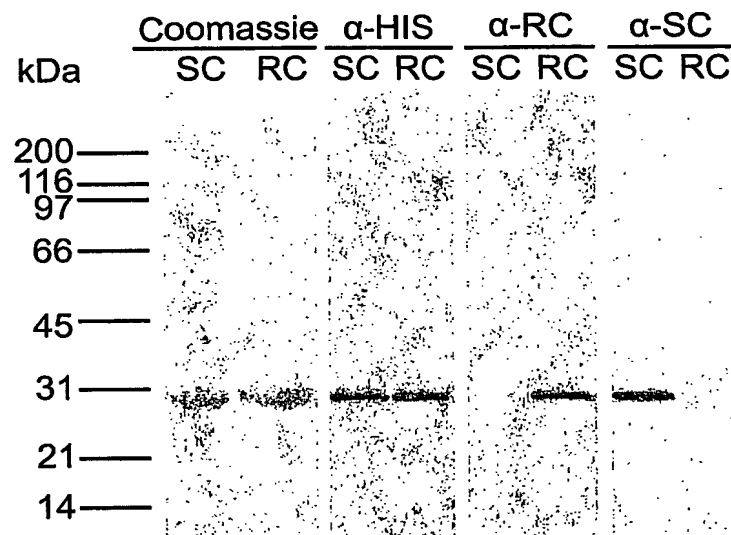


Figure 19B

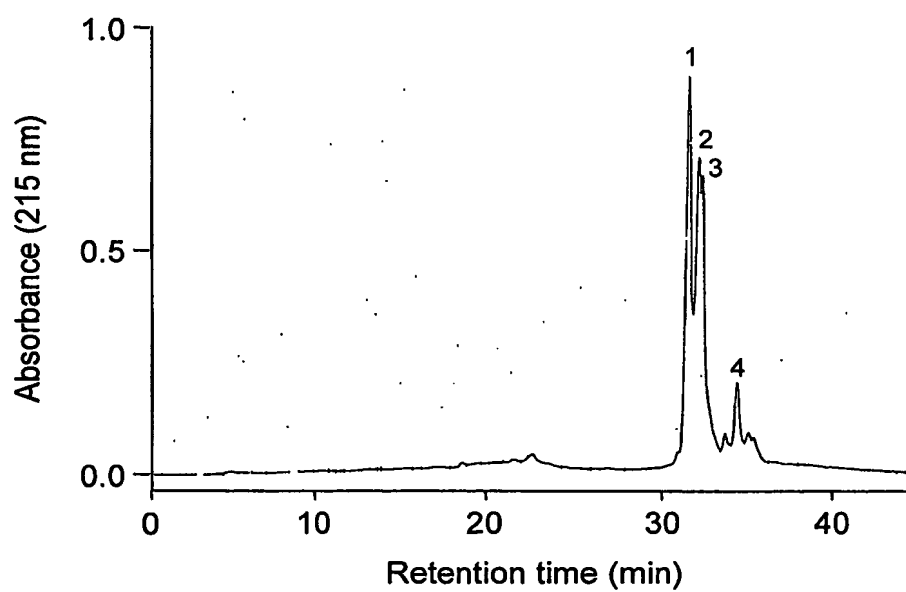
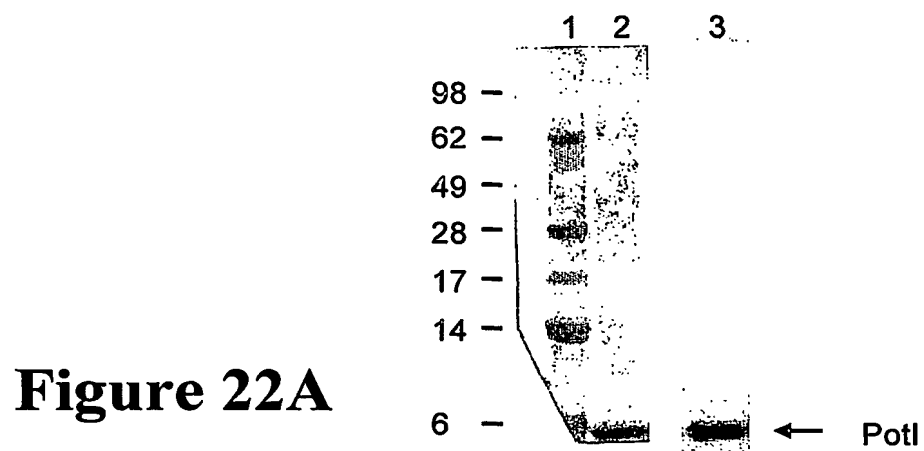
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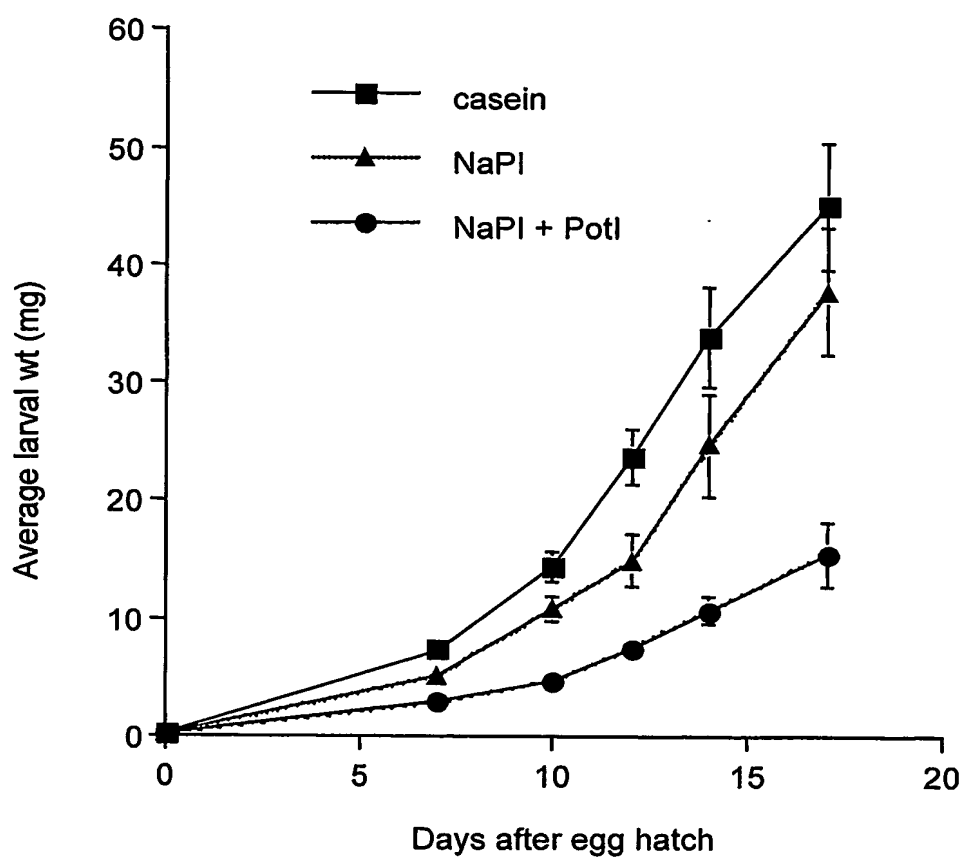
**Figure 20A****Figure 20B****Figure 20C**

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**Figure 21**

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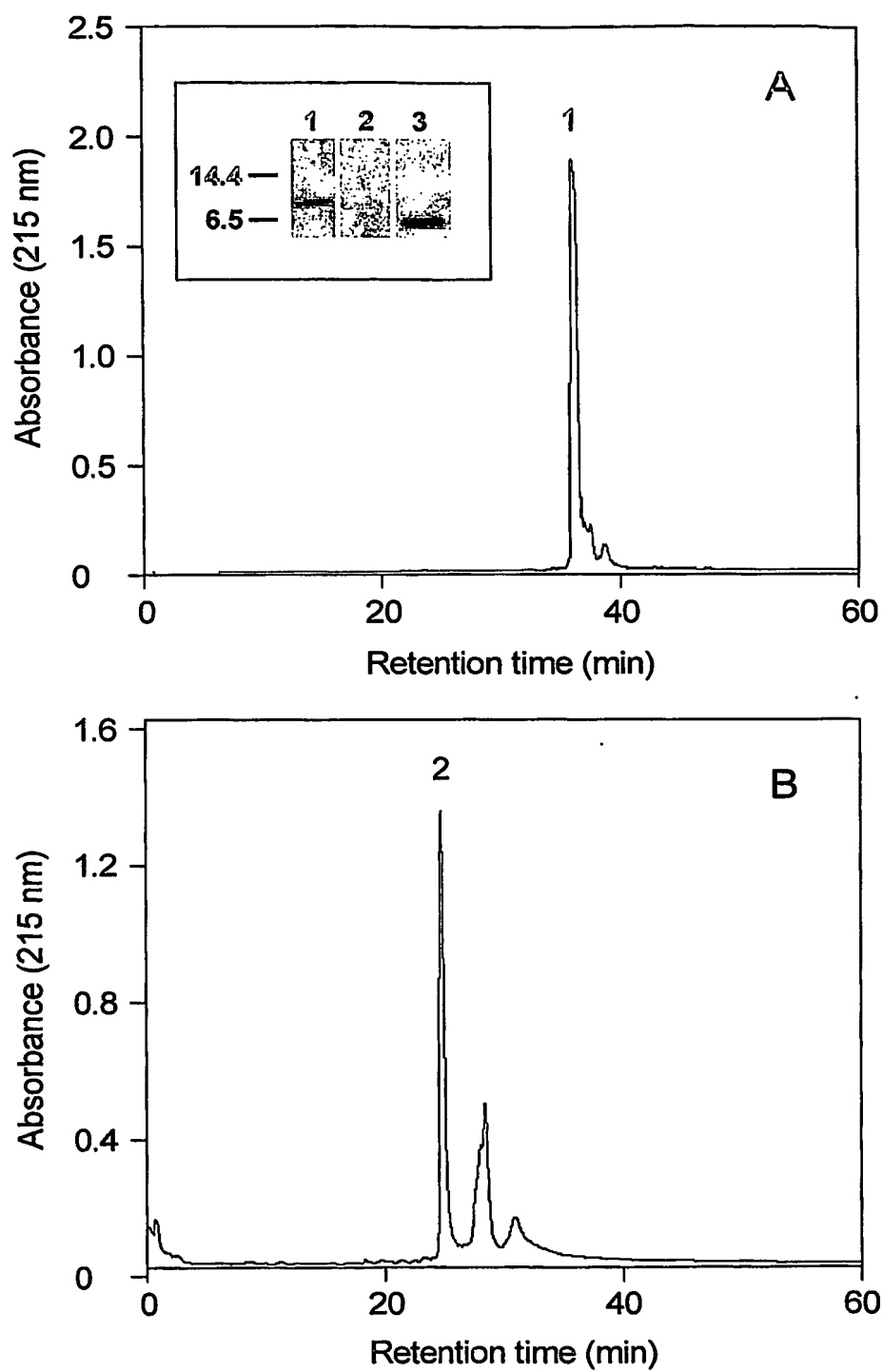


30/36**Figure 23**

[SEQ ID NO:77]	StPOTIB	1: MESKFAHIVVEFLLAHSFETLLARKESDGPEVEHEELKEFE	20	30	40	50	60
[SEQ ID NO:78]	X67950	1: MESKFAHIVVEFLLAHSFETLLARKESDGPEVEHEELKEFE				CNGKQFWPELIGVPTK:	56
[SEQ ID NO:79]	P01052	1:			KEFE	CDGKLQWPELIGVPTK:	20
[SEQ ID NO:80]	M17108	1: MESKFAHIVVEFLLAHSFETLLARKESDGPEVEHEELKEFE				CNGKQFWPELIGVPTK:	56
[SEQ ID NO:81]	StPOTIA	1: MESKFAHIVVEFLLAHSFETLLARKESDGSEVHKILKESES			SESW	CNGKQFWPELIGVPTK:	60
[SEQ ID NO:82]	K03290	1: MESKFAHIVVEFLLAHSFETLLARKESDGPEVEHEELKEFE			SNLM	CEGKQFWPELIGVPTK:	60
[SEQ ID NO:83]	Z12619	1: MVKFAHVAELLLASLIQPLTARDLEINVLDVQS			SGCP	GVTKERWPELIGVPTK:	56
[SEQ ID NO:84]	X78988	1:			STECGGG	GGKTSWPEVGSVE:	26
[SEQ ID NO:85]	EILXCH	1:			TEFG	SEIKSPEVCKTVD:	19

StPOTIB	57: LAKEIIEKENSLINNVOILLNGSPVTMDRCNRVRLFDNIIG	80	90	100	110
X67950	57: LAKEIIEKENSLINNVOILLNGSPVANDRCNRVRLFDNIIG				SVVQIPRVA: 107
P01052	21: LAKEIIEKONSLISNVHILLNGSPVTMDRCNRVRLFDNIIG				SVVQIPRVA: 107
M17108	57: LAKGIIEKENSLITNVQILLNGSPVTMDRCNRVRLFDNIIG				SVVQIPRVA: 71
StPOTIA	61: LAKEIIEKENPSINNVPIILLNGSPVPADRCNRVRLFDNIIG				DVVQIPRVA: 106
K03290	61: LAKEIIEKENPSITNNPIILLSGSPETEDVLCORVRLFDNIIG				DVVQIPRVA: 111
Z12619	57: FAMOLIIEKENPKTTNVQTELLNGSPVTEDLRNCRVRLFVNVLD				FVVQIPRVA: 111
X78988	27: DAKKVLKOKP.DADNVLPVGSVVTADLRNCRVRLFVNDI				FVVQIPRVA: 107
EILXCH	20: QAREYFTLHYP.QYDVFYELPEGSPVTEDLRNCRVRLFVNP				VAQTIPRVA: 73
					PHVG: 70

Figure 24

32/36**Figure 25**

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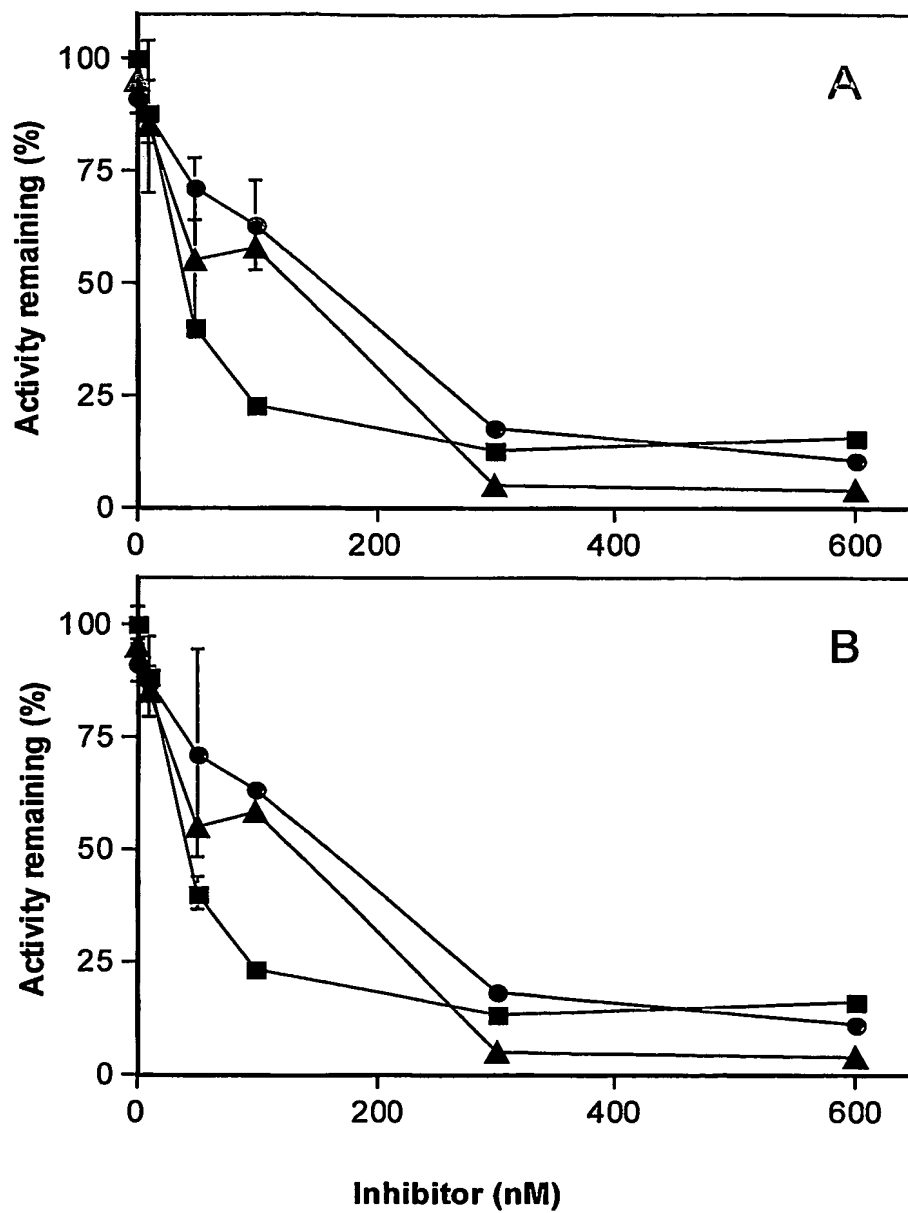
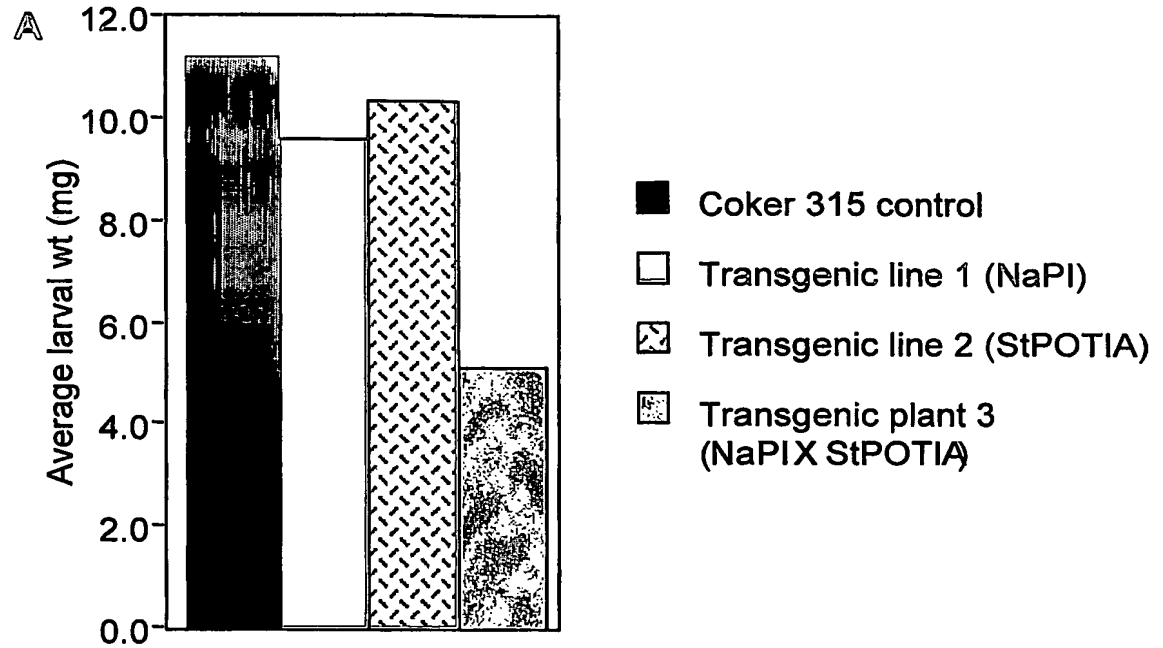
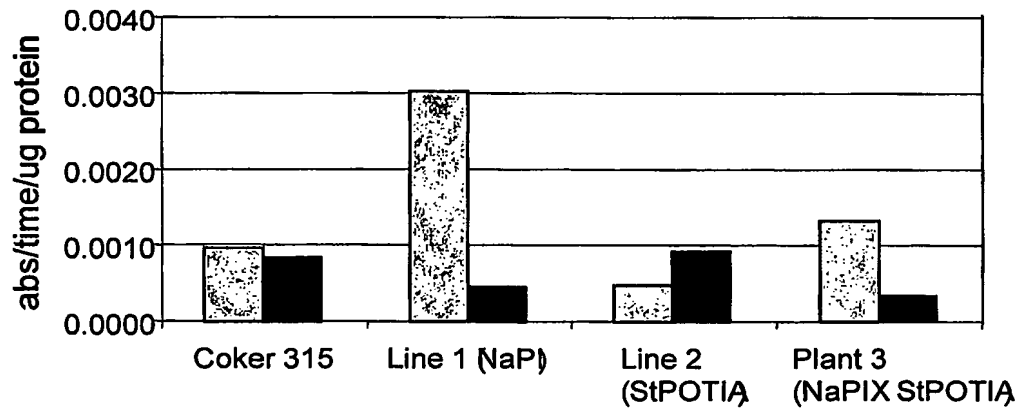


Figure 26

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**Figure 27A****Figure 27B**

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```

ggatccATGAAACTCTTGGCTGTGACTCTATTGGCTTTCGCCGCGGTTCGTCTCCGCGAGG      60
      M K L L A V T L L A F A A V V S A R

ggatccATGAAACTCTTGGCTGTGACTCTATTGGCtttcg
FwBacRECH2 Primer----->
                        TTGGCTTTCGCCGCGGTTCGTCTCCGCGAGG
                        FwBacRECH2 Primer-----

Aacgg [A] tcccaccatcaccatcaccatGTTACCTCGAGGATTCTATTGATCTGGAAGAT      120
      N G S H H H H H H V H L E D S I D L E D
Aacgg [G] tccc
----->

ATTACCGCTTGGGGATACCTCACCAAATTCGGTATTCCAGAAGCTGAGAAAATCCGCAAC      180
      I T A W G Y L T K F G I P E A E K I R N

GCTGAAGAAGCTAGCTCTGCTAGCAGGATCGTCGGTGGTTCATTGTCCAGTGTCCGACAG      240
      A E E A S S A S R I V G G S L S S V G Q

ATCCCTTACCAGGCTGGTCTCGTCATTGACTTAGCAGGTGGCCAGGCTGTCTGCGGAGGC      300
      I P Y Q A G L V I D L A G G Q A V C G G

TCCCTGATCAGCGCTTCCGCGTACTGACCGCTGCTCACTGCTGGTTCGACGGCCAAAAC      360
      S L I S A S R V L T A A H C W F D G Q N

CAGGCCTGGAGATTACCGTTGTTCTTGGTTCCACCACCTTGTTCTCTGGCGGTACCAGA      420
      Q A W R F T V V L G S T T L F S G G T R

ATCCCTACATCCAATGTTGTTATGCACGGAAGCTGGACTCCTAGCCTTATCCGTAACGAT      480
      I P T S N V V M H G S W T P S L I R N D

GTTGCCGTAATCAGATTGGGCACCAACGTAGCAACCTCAAACACCATTGCCATCATCGCT      540
      V A V I R L G T N V A T S N T I A I I A

CTACCCAGCGGCAGCCAGATCAACGAGAACTTCGCCGGTGAAACCGCCCTCGCCTCCGGC      600
      L P S G S Q I N E N F A G E T A L A S G

TTCGGTCTCACCAGTGACACCGGCAGCATCTCCAGCAACCAGGCTCTGAGCCACGTCAAC      660
      F G L T S D T G S I S S N Q A L S H V N

CTGCCAGTGATCACCAACGCTGTGTGCAGAAATTCATTCCCCCTGCTGATCCAGGACTCT      720
      L P V I T N A V C R N S F P L L I Q D S

AACATTTGCACCAGCGGTGCCAACGGCAGGAGCACTTGCCGCGGTGACTCCGGCGGTCCT      780
      N I C T S G A N G R S T C R G D S G G P

CTCGTCGTCACCAGGAACAACAGACCACTCTTGATCGGTATCACCTCTTTCGGATCTGCC      840
      L V V T R N N R P L L I G I T S F G S A

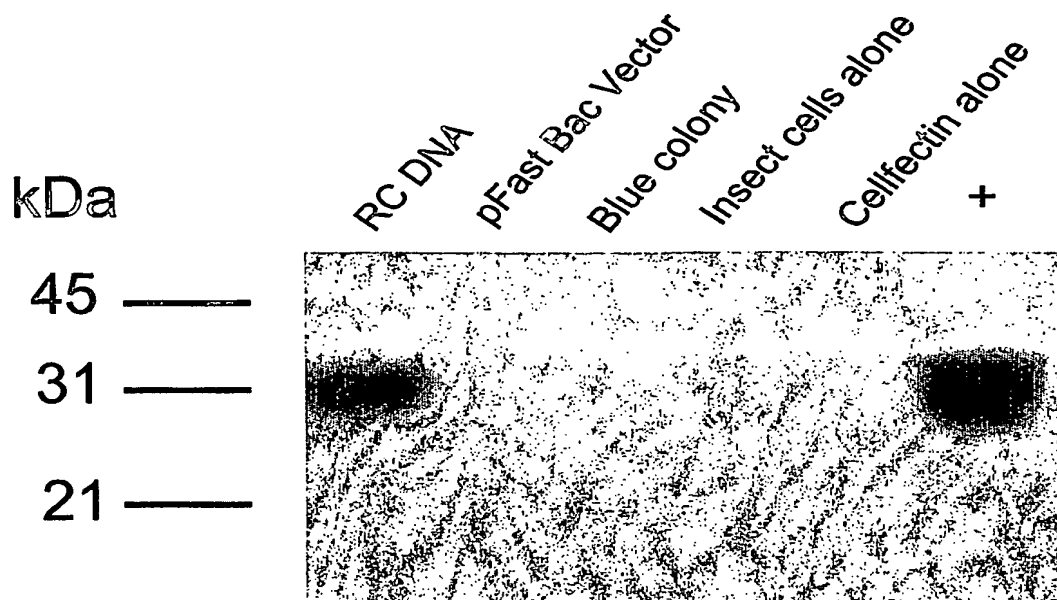
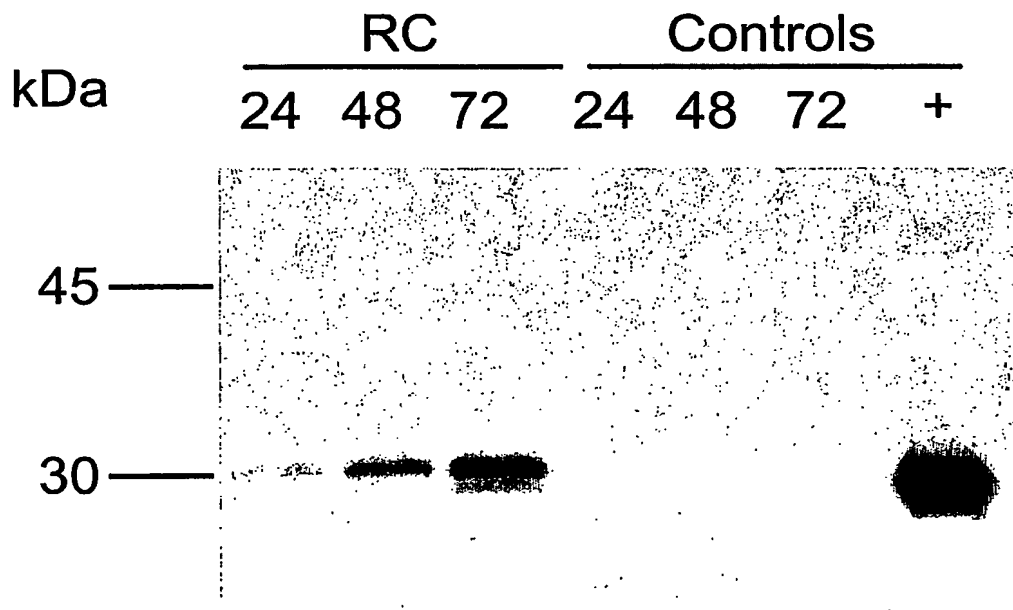
CGCGGTGCCAAGTTGGATCTCCCGCTGCCTTCGCCAGAGTCACCTCTTACATCAGCTG      900
      R G C Q V G S P A A F A R V T S Y I S W

GATCAACGGCCAGCTCTAAaagctt      925
      I N G Q L * K L

GATCAACGGCCAGCTCTAAaagctt
<-----RvRECH Primer

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Figure 28

36/36**Figure 29A****Figure 29B**

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